



## SEQUENCE LISTING

<110> Logemann, Juergen  
 Jach, Guido  
 Gornhardt, Birgit  
 Mundy, John  
 Schell, Jeff  
 Eckes, Peter  
 Chet, Ilan

<120> Transgenic pathogen-resistant organism

<130> A29542-FWC-I-R 070037.0195

<140> US 09/729,141

<141> 2000-12-01

<150> 08/812,025

<151> 1997-03-06

<150> 08/457,797

<151> 1995-06-01

<150> 08/134,416

<151> 1993-10-08

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 275

<212> DNA

<213> Aspergillus giganteus

<220>

<221> CDS

<222> (46)...(225)

<400> 1

ttgccacccc cggtgaagcc gattctctca ccgctggtgg tctgg atg caa gag atg 57  
 Met Gln Glu Met

1

aga gcg cgg gtt ttg gcc aca tac aat ggc aaa tgc tac aag aag gat 105  
 Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp  
 5 10 15 20

aat atc tgc aag tac aag gca cag agc ggc aag act gcc att tgc aag 153  
 Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys  
                   25                                  30                                  35

tgc tat gtc aaa aag tgc ccc cgc gac ggc gcg aaa tgc gag ttt gac 201  
 Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp  
                   40                                  45                                  50

agc tac aag ggg aag tgc tac tgc tagacggtga gcgaagggac gaagtaggct 255  
 Ser Tyr Lys Gly Lys Cys Tyr Cys  
                   55                                  60

ggggggttatt ttactctgct 275

<210> 2  
 <211> 60  
 <212> PRT  
 <213> *Aspergillus giganteus*

<400> 2  
 Met Gln Glu Met Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys  
   1                  5                                  10                                  15  
 Tyr Lys Lys Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr  
                   20                                  25                                  30  
 Ala Ile Cys Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys  
                   35                                  40                                  45  
 Cys Glu Phe Asp Ser Tyr Lys Gly Lys Cys Tyr Cys  
   50                                  55                                  60

<210> 3  
 <211> 51  
 <212> PRT  
 <213> *Aspergillus giganteus*

<400> 3  
 Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp Asn Ile Cys Lys Tyr  
   1                  5                                  10                                  15  
 Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys Cys Tyr Val Lys Lys  
                   20                                  25                                  30  
 Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp Ser Tyr Lys Gly Lys  
                   35                                  40                                  45  
 Cys Tyr Cys  
   50

<210> 4  
 <211> 1032  
 <212> DNA  
 <213> *Hordeum vulgare*

<220>  
 <221> 5'UTR  
 <222> (1)...(42)  
  
 <221> CDS  
 <222> (43)...(885)  
  
 <221> 3'UTR  
 <222> (886)...(1032)  
 <223> 46 nucleotides at the 3' end not shown  
  
 <221> polyA\_signal  
 <222> (930)...(935)  
 <223> potential polyadenylation signal  
  
 <221> polyA\_signal  
 <222> (963)...(976)  
 <223> potential polyadenylation signal  
  
 <221> polyA\_signal  
 <222> (1002)...(1011)  
 <223> potential polyadenylation signal  
  
 <221> mat\_peptide  
 <222> (46)...(886)

<400> 4  
 cttaatagca catcttgtcc gtcttagctt tgcattacat cc atg gcg gca aag 54  
 Met Ala Ala Lys  
 1  
  
 atg gcg aag aac gtg gac aag ccg ctc ttc acc gcg acg ttc aac gtc 102  
 Met Ala Lys Asn Val Asp Lys Pro Leu Phe Thr Ala Thr Phe Asn Val  
 5 10 15 20  
  
 cag gcc agc tcc gcc gac tac gcc acc ttc atc gcc ggc atc cgc aac 150  
 Gln Ala Ser Ser Ala Asp Tyr Ala Thr Phe Ile Ala Gly Ile Arg Asn  
 25 30 35  
  
 aag ctc cgc aac ccg gcg cac ttc tcc cac aac cgc ccc gtg ctg ccg 198  
 Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg Pro Val Leu Pro  
 40 45 50  
  
 ccg gtc gag ccc aac gtc ccg ccg agc agg tgg ttc cac gtc gtg ctc 246  
 Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe His Val Val Leu  
 55 60 65  
  
 aag gcc tcg ccg acc agc gcc ggg ctc acg ctg gcc att cgg gcg gac 294  
 Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala Ile Arg Ala Asp

70				75				80								
aac Asn 85	atc Ile	tac Tyr	ctg Leu	gag Glu	ggc Gly 90	ttc Phe	aag Lys	agc Ser	agc Ser	gac Asp 95	ggc Gly	acc Thr	tgg Trp	tgg Trp	gag Glu 100	342
ctc Leu	acc Thr	ccg Pro	ggc Gly	ctc Leu 105	atc Ile	ccc Pro	ggc Gly	gcc Ala	acc Thr 110	tac Tyr	gtc Val	ggg Gly	ttc Phe	ggc Gly 115	ggc Gly	390
acc Thr	tac Tyr	cgc Arg	gac Asp 120	ctc Leu	ctc Leu	ggc Gly	gac Asp	acc Thr 125	gac Asp	aag Lys	ctg Leu	acc Thr	aac Asn 130	gtc Val	gct Ala	438
ctc Leu	ggc Gly	cgg Arg 135	cag Gln	cag Gln	ctg Leu	gcg Ala	gac Asp 140	gcg Ala	gtg Val	acc Thr	gcc Ala	ctc Leu 145	cac His	ggg Gly	cgc Arg	486
acc Thr	aag Lys 150	gcc Ala	gac Asp	aag Lys	ccg Pro	tcc Ser 155	ggc Gly	ccg Pro	aag Lys	cag Gln	cag Gln 160	cag Gln	gcg Ala	agg Arg	gag Glu	534
gcg Ala 165	gtg Val	acg Thr	acg Thr	ctg Leu	ctc Leu 170	ctc Leu	atg Met	gtg Val	aac Asn	gag Glu 175	gcc Ala	acg Thr	cgg Arg	ttc Phe	cag Gln 180	582
acg Thr	gtg Val	tct Ser	ggg Gly	ttc Phe 185	gtg Val	gcc Ala	ggg Gly	ttg Leu	ctg Leu 190	cac His	ccc Pro	aag Lys	gcg Ala	gtg Val 195	gag Glu	630
aag Lys	aag Lys	agc Ser	ggg Gly 200	aag Lys	atc Ile	ggc Gly	aat Asn 205	gag Glu	atg Met	aag Lys	gcc Ala	cag Gln 210	gtg Val	aac Asn	ggg Gly	678
tgg Trp	cag Gln	gac Asp 215	ctg Leu	tcc Ser	gcg Ala	gcg Ala	ctg Leu 220	ctg Leu	aag Lys	acg Thr	gac Asp 225	gtg Val	aag Lys	cct Pro	ccg Pro	726
ccg Pro	gga Gly 230	aag Lys	tcg Ser	cca Pro	gcg Ala	aag Lys 235	ttc Phe	gcg Ala	ccg Pro	atc Ile	gag Glu 240	aag Lys	atg Met	ggc Gly	gtg Val	774
agg Arg 245	acg Thr	gct Ala	gta Val	cag Gln	gcc Ala 250	gcc Ala	aac Asn	acg Thr	ctg Leu	ggg Gly 255	atc Ile	ctg Leu	ctg Leu	ttc Phe	gtg Val 260	822
gag Glu	gtg Val	ccg Pro	ggt Gly	ggg Gly 265	ttg Leu	acg Thr	gtg Val	gcc Ala	aag Lys 270	gcg Ala	ctg Leu	gag Glu	ctg Leu	ttc Phe 275	cat His	870

gcg agt ggt ggg aaa taggtagttt tccaggtata cctgcatggg tagtgtaaaa 925  
Ala Ser Gly Gly Lys  
280

```
gtcgaataaaa catgtcacag agtgacggac tgatataaat aaataaataa acgtgtcaca 985
gagttacata taaacaaata aataaataat taaaaatgtc cagtttta 1032
```

```
<210> 5
<211> 281
<212> PRT
<213> Hordeum vulgare
```

<400>	5														
Met	Ala	Ala	Lys	Met	Ala	Lys	Asn	Val	Asp	Lys	Pro	Leu	Phe	Thr	Ala
1				5					10					15	
Thr	Phe	Asn	Val	Gln	Ala	Ser	Ser	Ala	Asp	Tyr	Ala	Thr	Phe	Ile	Ala
			20					25					30		
Gly	Ile	Arg	Asn	Lys	Leu	Arg	Asn	Pro	Ala	His	Phe	Ser	His	Asn	Arg
		35					40					45			
Pro	Val	Leu	Pro	Pro	Val	Glu	Pro	Asn	Val	Pro	Pro	Ser	Arg	Trp	Phe
	50					55					60				
His	Val	Val	Leu	Lys	Ala	Ser	Pro	Thr	Ser	Ala	Gly	Leu	Thr	Leu	Ala
65					70					75					80
Ile	Arg	Ala	Asp	Asn	Ile	Tyr	Leu	Glu	Gly	Phe	Lys	Ser	Ser	Asp	Gly
				85					90					95	
Thr	Trp	Trp	Glu	Leu	Thr	Pro	Gly	Leu	Ile	Pro	Gly	Ala	Thr	Tyr	Val
			100					105					110		
Gly	Phe	Gly	Gly	Thr	Tyr	Arg	Asp	Leu	Leu	Gly	Asp	Thr	Asp	Lys	Leu
		115					120					125			
Thr	Asn	Val	Ala	Leu	Gly	Arg	Gln	Gln	Leu	Ala	Asp	Ala	Val	Thr	Ala
	130					135					140				
Leu	His	Gly	Arg	Thr	Lys	Ala	Asp	Lys	Pro	Ser	Gly	Pro	Lys	Gln	Gln
145					150					155					160
Gln	Ala	Arg	Glu	Ala	Val	Thr	Thr	Leu	Leu	Leu	Met	Val	Asn	Glu	Ala
				165					170					175	
Thr	Arg	Phe	Gln	Thr	Val	Ser	Gly	Phe	Val	Ala	Gly	Leu	Leu	His	Pro
			180				185						190		
Lys	Ala	Val	Glu	Lys	Lys	Ser	Gly	Lys	Ile	Gly	Asn	Glu	Met	Lys	Ala
		195					200					205			
Gln	Val	Asn	Gly	Trp	Gln	Asp	Leu	Ser	Ala	Ala	Leu	Leu	Lys	Thr	Asp
	210					215					220				
Val	Lys	Pro	Pro	Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Ala	Pro	Ile	Glu
225					230					235					240
Lys	Met	Gly	Val	Arg	Thr	Ala	Val	Gln	Ala	Ala	Asn	Thr	Leu	Gly	Ile
				245					250					255	
Leu	Leu	Phe	Val	Glu	Val	Pro	Gly	Gly	Leu	Thr	Val	Ala	Lys	Ala	Leu
			260					265					270		
Glu	Leu	Phe	His	Ala	Ser	Gly	Gly	Lys							
		275					280								

<210> 6  
 <211> 480  
 <212> DNA  
 <213> Hordeum vulgare

<220>  
 <221> CDS  
 <222> (1)...(351)  
 <223> protein synthetis inhibitor (PSI), aminoterminally  
 incomplete protein from an incomplete PSI cDNA  
 clone

<221> 3'UTR  
 <222> (352)...(487)

<221> polyA\_signal  
 <222> (404)...(409)  
 <223> potential polyadenylation signal

<221> polyA\_signal  
 <222> (437)...(442)  
 <223> potential polyadenylation signal

<221> polyA\_signal  
 <222> (445)...(450)  
 <223> potential polyadenylation signal

<400> 6  
 gcg gtg acg acg ctg ctc ctc atg gtg aac gag gcc acg cgg ttc cag 48  
 Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln  
 1 5 10 15  
 acg gtg tcg ggg ttc gtg gcc ggg ctg ctg cac ccc aag gcg gtg gag 96  
 Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu  
 20 25 30  
 aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg 144  
 Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly  
 35 40 45  
 tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag ccc ccg 192  
 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro  
 50 55 60  
 ccg gga aag tcg cca gcg aag ttc acg ccg atc gag aag atg ggc gtg 240  
 Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val  
 65 70 75 80  
 agg act gct gag cag gct gcg gct act ttg ggg atc ctg ctg ttc gtt 288

Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val  
                     85                    90                    95

gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttt cat 336  
 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His  
                     100                    105                    110

gcg agt ggt ggg aaa taggtagttt tgcaggtata cctgcatggg taaatgtaaa 391  
 Ala Ser Gly Gly Lys  
                     115

agtcgaataa aaatgtcaca gagtgacgga ctgatataaa taaattaata aacatgtcat 451  
 catgagtgac agactgatat aaataaata 480

<210> 7

<211> 117

<212> PRT

<213> Hordeum vulgare

<400> 7

Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln  
 1                    5                    10                    15  
 Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu  
                     20                    25                    30  
 Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly  
                     35                    40                    45  
 Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro  
                     50                    55                    60  
 Pro Gly Lys Ser Pro Ala Lys Phe Thr Pro Ile Glu Lys Met Gly Val  
 65                    70                    75                    80  
 Arg Thr Ala Glu Gln Ala Ala Ala Thr Leu Gly Ile Leu Leu Phe Val  
                     85                    90                    95  
 Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His  
                     100                    105                    110  
 Ala Ser Gly Gly Lys  
                     115

<210> 8

<211> 2329

<212> DNA

<213> Serratia marcescens

<220>

<221> misc\_feature

<222> (1)...(2329)

<223> ChiS gene from plasmid pLChis from E.coli A5187

<400> 8

cagggcgttg tcaataatga caacaccctg gctgaagagt gtggtgcaat actgataaat 60

```

atztatcttt ccttaataga aaattcacta tccttatttg tcatgttttc ttttatttat 120
atgaaaataa attcacgctt gctgaataaa acccagttga tagcgctctt gtttttgcgc 180
cttttttatt tatagtactg aatgtacgcg gtgggaatga ttatttcgcc acgtggaaag 240
acgctgttgt tatttattga ttttaacctt cgcggattat tgcggaattt tttcgcttcg 300
gcaatgcata gcgacgatta actcttttat gtttatcctc tcggaataaa ggaatcagtt 360
atgcgcaaata ttaataaacc gctgttgagg ctgttgatcg gcagcacgct gtgttcgcgc 420
gcgcaggccg ccgcgccggg caagccgacc atcgccctggg gcaacaccaa gttcgccatc 480
gttgaagttg accaggcggc taccgcttat aataatttg tgaaggtaaa aaatgccgcc 540
gatgtttccg tctcctggaa tttatggaat ggcgacaccg gcacgacggc aaaagtttta 600
ttaaatggca aagaggcgtg gagtggctct tcaaccggat cttccggtac ggcgaatttt 660
aaagtgaata aaggcggccg ttatcaaatg caggtggcac tgtgcaatgc cgacggctgc 720
accgccagtg acgccaccga aattgtggta gccgacaccg acggcagcca tttggcgccg 780
ttgaaagagc cgctgctgga aaagaataaa ccgtataaac agaactccgg caaagtggtc 840
ggttcttatt tcgtcgagtg gggcggtttac gggcgcaatt tcaccgtcga caagatcccg 900
gcgcaaaacc tgaccacact gctgtacggc tttatcccga tctgcggcgc caatggcatc 960
aacgacagcc tgaaagagat tgaaggcagc ttccaggcgt tgcagcgctc ctgccagggc 1020
cgcgaggact tcaaagtctc gatccacgat ccgttcgccc cgctgcaaaa agcgcagaag 1080
ggcgtgaccg cctgggatga ccctacaag ggcaacttcg gccagctgat ggcgctgaag 1140
caggcgcata ctgacctgaa aatcctgccg tcgatcggcg gctggacgct gtccgacccg 1200
ttcttcttca tgggcgacaa ggtgaagcgc gatcgcttcg tcggttcggt gaaagagttc 1260
ctgcagacct ggaagttctt cgacggcgtg gatatcgact gggagttccc gggcggcaaa 1320
ggcgccaacc ctaacctggg cagcccgcga gacggggaaa cctatgtgct gctgatgaag 1380
gagctgcggg cgatgctgga tcagctgtcg gtggaaaccg gccgcaagta tgagctgacc 1440
tccgccatca gcgccggtaa ggacaagatc gacaagggtg cttacaacgt tgcgcagaac 1500
tcgatggatc acatcttcct gatgagctac gacttctatg gcgccttcga tctgaagaac 1560
ctggggcata agaccgcgct gaatgcgccg gcctggaaac cggacaccgc ctacaccacg 1620
gtgaacggcg tcaatgcgct gctggcgcgag ggcgtcaagc cgggcaaaat cgtcgtcggc 1680
accgccatgt atggccgcgg ctggaccggg gtgaacggct accagaacaa tattccgttc 1740
accggcaccg ccaccggggc ggttaaaggc acctgggaga acggtatcgt ggactaccgc 1800
caaatcgccg gccagttcat gagcggcgag tggcagtata cctacgacgc cacggcggaa 1860
gcgccttacg tggtcaaacc ttccaccggc gatctgatca ctttcgacga tgcccgtcgc 1920
gtgcaggcta aaggcaagta cgtgttgat aagcagctgg gcggcctgtt ctccctgggag 1980
atcgacgcgg ataacggcga tattctcaac agcatgaacg ccagcctggg caacagcgcc 2040
ggcgttcaat aatcggttgc agtggttgcc gggggatata ctttcgcccc cggctttttc 2100
gccgacgaaa gtttttttac gccgcacaga ttgtggctct gccccgagca aaacgcgctc 2160
atcggactca cccttttggg taatccttca gcatttcctc ctgtctttaa cggcgatcac 2220
aaaaataacc gttcagatat tcatcattca gcaacaaagt tttggcgttt ttttaacggag 2280
ttaaaaacca gtaagtttgt gagggtcaga ccaatgcgct aaaaatggg 2329

```

<210> 9  
 <211> 1002  
 <212> DNA  
 <213> *Hordeum vulgare*

<220>  
 <221> 5'UTR  
 <222> (1)... (63)

<221> CDS  
 <222> (64)... (861)



<223> 26 kD preprotein of chitinase (ChiG)

<221> 3'UTR

<222> (862)...(1002)

<223> partial, 11 nucleotides at 3' end not shown

<221> polyA\_signal

<222> (905)...(910)

<223> potential polyadenylation site

<221> sig\_peptide

<222> (64)...(294)

<223> probable signal peptide

<221> sig\_peptide

<222> (298)...(312)

<223> probable signal peptide

<221> sig\_peptide

<222> (349)...(378)

<223> probable signal peptide

<221> sig\_peptide

<222> (466)...(588)

<223> probable signal peptide

<221> sig\_peptide

<222> (607)...(861)

<223> probable signal peptide

<221> mat\_peptide

<222> (133)...(861)

<400> 9

cctacgacag tagcgtaacg gtaaacaccg agtacggtac tctgtgcttt gttggctcgc 60

aca atg aga tcg ctc gcg gtg gtg gtg gcc gtg gta gcc acg gtg gcc 108

Met Arg Ser Leu Ala Val Val Val Ala Val Val Ala Thr Val Ala

1

5

10

15

atg gcc atc ggc acg gcg cgc ggc agc gtg tcc tcc atc gtc tcg cgc 156

Met Ala Ile Gly Thr Ala Arg Gly Ser Val Ser Ser Ile Val Ser Arg

20

25

30

gca cag ttt gac cgc atg ctt ctc cac cgc aac gac ggc gcc tgc cag 204

Ala Gln Phe Asp Arg Met Leu Leu His Arg Asn Asp Gly Ala Cys Gln

35

40

45

gcc aag ggc ttc tac acc tac gac gcc ttc gtc gcc gcc gca gcc gcc 252

Ala Lys Gly Phe Tyr Thr Tyr Asp Ala Phe Val Ala Ala Ala Ala Ala

50

55

60

ttc ccg ggc ttc ggc acc acc ggc agc gcc gac gcc cag aag cgc gag	300
Phe Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Ala Gln Lys Arg Glu	
65 70 75	
gtg gcc gcc ttc cta gca cag acc tcc cac gag acc acc ggc ggg tgg	348
Val Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr Thr Gly Gly Trp	
80 85 90 95	
gcg act gca ccg gac ggg gcc ttc gcc tgg ggc tac tgc ttc aag cag	396
Ala Thr Ala Pro Asp Gly Ala Phe Ala Trp Gly Tyr Cys Phe Lys Gln	
100 105 110	
gaa cgt ggc gcc tcc tcc gac tac tgc acc ccg agc gca caa tgg ccg	444
Glu Arg Gly Ala Ser Ser Asp Tyr Cys Thr Pro Ser Ala Gln Trp Pro	
115 120 125	
tgc gcc ccc ggg aag cgc tac tac ggc cgc ggg cca atc cag ctc tcc	492
Cys Ala Pro Gly Lys Arg Tyr Tyr Gly Arg Gly Pro Ile Gln Leu Ser	
130 135 140	
cac aac tac aac tat gga cct gcc ggc cgg gcc atc ggg gtc gat ctg	540
His Asn Tyr Asn Tyr Gly Pro Ala Gly Arg Ala Ile Gly Val Asp Leu	
145 150 155	
ctg gcc aac ccg gac ctg gtg gcc acg gac gcc act gtg ggc ttt aag	588
Leu Ala Asn Pro Asp Leu Val Ala Thr Asp Ala Thr Val Gly Phe Lys	
160 165 170 175	
acg gcc atc tgg ttc tgg atg acg gcg cag ccg ccc aag cca tcg agc	636
Thr Ala Ile Trp Phe Trp Met Thr Ala Gln Pro Pro Lys Pro Ser Ser	
180 185 190	
cat gct gtg atc gcc ggc cag tgg agc ccg tca ggg gct gac cgg gcc	684
His Ala Val Ile Ala Gly Gln Trp Ser Pro Ser Gly Ala Asp Arg Ala	
195 200 205	
gca ggc cgg gtg ccc ggg ttt ggt gtg atc acc aac atc atc aac ggc	732
Ala Gly Arg Val Pro Gly Phe Gly Val Ile Thr Asn Ile Ile Asn Gly	
210 215 220	
ggg atc gag tgc ggt cac ggg cag gac agc cgc gtc gcc gat cga atc	780
Gly Ile Glu Cys Gly His Gly Gln Asp Ser Arg Val Ala Asp Arg Ile	
225 230 235	
ggg ttt tac aag cgc tac tgt gac atc ctc ggc gtt ggc tac ggc aac	828
Gly Phe Tyr Lys Arg Tyr Cys Asp Ile Leu Gly Val Gly Tyr Gly Asn	



<400> 10															
Met	Arg	Ser	Leu	Ala	Val	Val	Val	Ala	Val	Val	Ala	Thr	Val	Ala	Met
1				5					10					15	
Ala	Ile	Gly	Thr	Ala	Arg	Gly	Ser	Val	Ser	Ser	Ile	Val	Ser	Arg	Ala
			20					25					30		
Gln	Phe	Asp	Arg	Met	Leu	Leu	His	Arg	Asn	Asp	Gly	Ala	Cys	Gln	Ala
		35					40					45			
Lys	Gly	Phe	Tyr	Thr	Tyr	Asp	Ala	Phe	Val	Ala	Ala	Ala	Ala	Ala	Phe
	50					55					60				
Pro	Gly	Phe	Gly	Thr	Thr	Gly	Ser	Ala	Asp	Ala	Gln	Lys	Arg	Glu	Val
65					70					75					80
Ala	Ala	Phe	Leu	Ala	Gln	Thr	Ser	His	Glu	Thr	Thr	Gly	Gly	Trp	Ala
				85					90					95	
Thr	Ala	Pro	Asp	Gly	Ala	Phe	Ala	Trp	Gly	Tyr	Cys	Phe	Lys	Gln	Glu
			100					105					110		
Arg	Gly	Ala	Ser	Ser	Asp	Tyr	Cys	Thr	Pro	Ser	Ala	Gln	Trp	Pro	Cys
		115					120					125			
Ala	Pro	Gly	Lys	Arg	Tyr	Tyr	Gly	Arg	Gly	Pro	Ile	Gln	Leu	Ser	His
	130					135					140				
Asn	Tyr	Asn	Tyr	Gly	Pro	Ala	Gly	Arg	Ala	Ile	Gly	Val	Asp	Leu	Leu
145					150					155					160
Ala	Asn	Pro	Asp	Leu	Val	Ala	Thr	Asp	Ala	Thr	Val	Gly	Phe	Lys	Thr
				165					170					175	
Ala	Ile	Trp	Phe	Trp	Met	Thr	Ala	Gln	Pro	Pro	Lys	Pro	Ser	Ser	His
			180					185					190		
Ala	Val	Ile	Ala	Gly	Gln	Trp	Ser	Pro	Ser	Gly	Ala	Asp	Arg	Ala	Ala
		195					200				205				
Gly	Arg	Val	Pro	Gly	Phe	Gly	Val	Ile	Thr	Asn	Ile	Ile	Asn	Gly	Gly
	210					215					220				
Ile	Glu	Cys	Gly	His	Gly	Gln	Asp	Ser	Arg	Val	Ala	Asp	Arg	Ile	Gly
225					230					235					240
Phe	Tyr	Lys	Arg	Tyr	Cys	Asp	Ile	Leu	Gly	Val	Gly	Tyr	Gly	Asn	Asn
				245					250					255	
Leu	Asp	Cys	Tyr	Ser	Gln	Arg	Pro	Phe	Ala						
			260					265							

<210> 11  
 <211> 1235  
 <212> DNA  
 <213> Hordeum vulgare

<220>  
 <221> 5'UTR  
 <222> (1)...(48)

<221> CDS  
 <222> (49)...(1050)  
 <223> preprotein of the glucanase GluG

<221> 3'UTR  
 <222> (1051)...(1235)  
 <223> partial, 14 nucleotides at the 3' end not shown

<221> polyA\_signal  
 <222> (1083)...(1088)  
 <223> potential polyadenylation signal

<221> polyA\_signal  
 <222> (1210)...(1215)  
 <223> potential polyadenylation signal

<221> mat\_peptide  
 <222> (133)...(1050)

<400> 11  
 ggcagcattg catagcattt gagcaccaga tactccgtgt gtgcacca atg gct aga 57  
 Met Ala Arg  
 1

aaa gat gtt gcc tcc atg ttt gca gtt gct ctc ttc att gga gca ttc 105  
 Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile Gly Ala Phe  
 5 10 15

gct gct gtt cct acg agt gtg cag tcc atc ggc gta tgc tac ggc gtg 153  
 Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys Tyr Gly Val  
 20 25 30 35

atc ggc aac aac ctc ccc tcc cgg agc gac gtg gtg cag ctc tac agg 201  
 Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln Leu Tyr Arg  
 40 45 50

tcc aag ggc atc aac ggc atg cgc atc tac ttc gcc gac ggg cag gcc 249  
 Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp Gly Gln Ala  
 55 60 65



Ser Gly Trp Pro Ser Ala Gly Gly Phe Ala Ala Ser Ala Gly Asn Ala  
 260 265 270 275

cgg acg tac aac cag ggg ctg atc aac cac gtc ggc ggg ggc acg ccc 921  
 Arg Thr Tyr Asn Gln Gly Leu Ile Asn His Val Gly Gly Gly Thr Pro  
 280 285 290

aag aag cgg gag gcg ctg gag acg tac atc ttc gcc atg ttc aac gag 969  
 Lys Lys Arg Glu Ala Leu Glu Thr Tyr Ile Phe Ala Met Phe Asn Glu  
 295 300 305

aac cag aag acc ggg gac gcc acg gag agg agc ttc ggg ctc ttc aac 1017  
 Asn Gln Lys Thr Gly Asp Ala Thr Glu Arg Ser Phe Gly Leu Phe Asn  
 310 315 320

ccg gac aag tcg ccg gca tac aac atc cag ttc tagtacgtgt agctacctag 1070  
 Pro Asp Lys Ser Pro Ala Tyr Asn Ile Gln Phe  
 325 330

ctcacatacc taaataaata agctgcacgt acgtacgtaa tgcggcatcc aagtgtaacg 1130  
 tagacacgta cattcatcca tggaagagtg caaccaagca tgcgttaact tcctggtgat 1190  
 gatacatcat catggtatga ataaaagata tggaagatgt tatga 1235

<210> 12

<211> 334

<212> PRT

<213> Hordeum vulgare

<400> 12

Met Ala Arg Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile  
 1 5 10 15  
 Gly Ala Phe Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys  
 20 25 30  
 Tyr Gly Val Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln  
 35 40 45  
 Leu Tyr Arg Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp  
 50 55 60  
 Gly Gln Ala Leu Ser Ala Val Arg Asn Ser Gly Ile Gly Leu Ile Leu  
 65 70 75 80  
 Asp Ile Gly Asn Asp Gln Leu Ala Asn Ile Ala Ala Ser Thr Ser Asn  
 85 90 95  
 Ala Ala Ser Trp Val Gln Asn Asn Val Arg Pro Tyr Tyr Pro Ala Val  
 100 105 110  
 Asn Ile Lys Tyr Ile Ala Ala Gly Asn Glu Val Gln Gly Gly Ala Thr  
 115 120 125  
 Gln Ser Ile Leu Pro Ala Met Arg Asn Leu Asn Ala Ala Leu Ser Ala  
 130 135 140  
 Ala Gly Leu Gly Ala Ile Lys Val Ser Thr Ser Ile Arg Phe Asp Glu  
 145 150 155 160  
 Val Ala Asn Ser Phe Pro Pro Ser Ala Gly Val Phe Lys Asn Ala Tyr

				165					170				175			
Met	Thr	Asp	Val	Ala	Arg	Leu	Leu	Ala	Ser	Thr	Gly	Ala	Pro	Leu	Leu	
			180					185					190			
Ala	Asn	Val	Tyr	Pro	Tyr	Phe	Ala	Tyr	Arg	Asp	Asn	Pro	Gly	Ser	Ile	
		195					200					205				
Ser	Leu	Asn	Tyr	Ala	Thr	Phe	Gln	Pro	Gly	Thr	Thr	Val	Arg	Asp	Gln	
	210					215					220					
Asn	Asn	Gly	Leu	Thr	Tyr	Thr	Ser	Leu	Phe	Asp	Ala	Met	Val	Asp	Ala	
225					230					235					240	
Val	Tyr	Ala	Ala	Leu	Glu	Lys	Ala	Gly	Ala	Pro	Ala	Val	Lys	Val	Val	
			245					250						255		
Val	Ser	Glu	Ser	Gly	Trp	Pro	Ser	Ala	Gly	Gly	Phe	Ala	Ala	Ser	Ala	
			260					265					270			
Gly	Asn	Ala	Arg	Thr	Tyr	Asn	Gln	Gly	Leu	Ile	Asn	His	Val	Gly	Gly	
	275						280					285				
Gly	Thr	Pro	Lys	Lys	Arg	Glu	Ala	Leu	Glu	Thr	Tyr	Ile	Phe	Ala	Met	
	290					295					300					
Phe	Asn	Glu	Asn	Gln	Lys	Thr	Gly	Asp	Ala	Thr	Glu	Arg	Ser	Phe	Gly	
305					310					315					320	
Leu	Phe	Asn	Pro	Asp	Lys	Ser	Pro	Ala	Tyr	Asn	Ile	Gln	Phe			
				325					330							